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10 APR 2003

L1 0 S BETA ACTIN CAP73  
L2 9 S BETA CAP73  
L3 3 DUP REM L2 (6 DUPLICATES REMOVED)

L Number	Hits	Search Text	DB	Time stamp
1	0	beta adj actin adj cap73	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/10 09:44
2	0	bcap73	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/10 09:44
3	0	\$cap73	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/04/10 09:44

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# NiceProt View of TrEMBL: Q8HYY4

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## General information about the entry

Entry name	Q8HYY4
Primary accession number	Q8HYY4
Secondary accession numbers	None
Entered in TrEMBL in	Release 23, March 2003
Sequence was last modified in	Release 23, March 2003
Annotations were last modified in	Release 24, June 2003

## Name and origin of the protein

Protein name	Beta-actin binding protein betaCAP73
Synonyms	None
Gene name	None
From	<a href="#">Bos taurus (Bovine) [TaxID: 9913]</a>
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Cetartiodactyla</a> ; <a href="#">Ruminantia</a> ; <a href="#">Pecora</a> ; <a href="#">Bovoidea</a> ; <a href="#">Bovidae</a> ; <a href="#">Bovinae</a> ; <a href="#">Bos</a> .

## References

[1] SEQUENCE FROM NUCLEIC ACID.  
 MEDLINE=21947821; PubMed=11950601; [\[NCBI\]](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)  
 Welch A.Y., Herman I.M.;  
 "Cloning and characterization of betaCAP73, a novel regulator of beta-actin assembly.";  
 Int. J. Biochem. Cell Biol. 34:864-881(2002).

## Comments

None

## Cross-references

EMBL	<a href="#">AY152693</a> ; <a href="#">AAN74017.1</a> ; -.	<a href="#">[EMBL]</a> <a href="#">[GenBank]</a> <a href="#">[DDBJ]</a> <a href="#">[CoDingSequence]</a>
InterPro	<a href="#">IPR002110</a> ; ANK.	<a href="#">[Graphical view of domain structure]</a>
Pfam	PF00023; ank; 6.	
SMART	SM00248; ANK; 6.	
PROSITE	PS50088; ANK_REPEAT; 5.	
ProDom	PS50297; ANK REP REGION; 1.	<a href="#">[Domain structure / List of seq. sharing at least 1 domain]</a>
ProtoMap	Q8HYY4.	
PRESAGE	Q8HYY4.	
ModBase	Q8HYY4.	
SWISS-2DPAGE	Get region on 2D PAGE	

## Keywords

None

## Features

None

## Sequence information

Length: 1401 AA Molecular weight: 161298 Da CRC64: 429312A3F658546A [This is a checksum on the sequence]

10	20	30	40	50	60
MMSCWFSCAP	KNRQAADWNK	YDDRLMRAAE	RGDVEKVSSI	LAKKGVNPGK	LDVEGRSAFH
70	80	90	100	110	120
VVASKGNLEC	LNAILIHGV	ITTSDTAGRN	ALHLAAKYGH	ALCLOKLLQY	NCPTEHVVDLQ
130	140	150	160	170	180
GRTALHDAAM	ADCPSSIQLL	CDHGASVNAK	DVDGRTPLVL	ATQMCRPTIC	QLLIDRGADI
190	200	210	220	230	240
NSRDKQNR	LMLGCEYGCK	DAVEVLIKNG	ADVTLDDALG	HDSSYYARIG	DNLDILTLK
250	260	270	280	290	300
TASENSNKGR	ELWKKGPSLQ	QRNLSQLMDE	VNTKSNOREH	QNIQDLEIEN	EDLKERLRKI
310	320	330	340	350	360
QQEQRILLDK	VNGLQLQLNE	EVMVADDLES	EKEKLKSLLA	AKEQHEESL	RTIEALKSRF
370	380	390	400	410	420
KYFESDHLGS	GSHFRKEDML	LKQGQMYMTD	SQCTSTGMPV	HMQSRSMLRP	LELALPNQAS
430	440	450	460	470	480
YSENEILKKE	LEAMRTFCDS	AKQDRLKLQN	ELAHKVAECK	ALALECERVK	EDSDEQIKQL
490	500	510	520	530	540
EDALKDVQKR	MYESEGKVVKQ	MQTHFLFLAK	HLTSDAATGN	HRLMEELKDQ	LKDMKVVKYEG
550	560	570	580	590	600
ASAEVGKLRN	QIKQNEMLVE	EFKRDEGKLM	EENKRLQKEL	SMCELEREKR	GRKLTEMEGQ
610	620	630	640	650	660
LKDLSAKLAL	SIPAEEKFENM	KSLLSNELNE	KAKKLIDVER	EYERSLNETR	PLKRELENLK
670	680	690	700	710	720
AKLAQHVKPE	EHEQLKSRLE	QKSGELGKRI	TELTSKNQTL	QKEIEKVCLD	NKLLTQQVNN
730	740	750	760	770	780
LTTEMKNHYV	PLKVSEEMKK	SHDVIVDDLN	KKLSDVTHKY	TEKKLEMEKL	LMENASLSKN
790	800	810	820	830	840
VSRLETVFIP	PERHEKEMMA	LKSNNITELKK	QLSELNKKCG	EDQEKEIYSLM	SENNDLKKT
850	860	870	880	890	900
SHQYVPVKTH	EEIKTALSST	LDKTNRELVD	VKKKCEDINQ	EFVKIKDENE	ILKRNLENTQ
910	920	930	940	950	960

NQVKA <del>Y</del> ISL	REHEEKMSG <del>L</del>	RKSMKKVQDN	SAEILAKYKK	SQEEIVTLHE	EIAAQKRELD
970	980	990	1000	1010	1020
TIQECIKLKY	APIISLEECE	RKF <del>KATE</del> KEL	KEQLSQQTQK	YNT <del>SEE</del> EAKK	CKQENDKLKK
1030	1040	1050	1060	1070	1080
EILTLQKDLK	DKNVHIENSY	ETERALSRKT	EELNRQLKDL	LQKYTEAKKE	KEKLVEENAK
1090	1100	1110	1120	1130	1140
QTSEILAAQT	LLQKQHVPLE	QVESLKKSL <del>S</del>	GTIETLKEEL	KTKQRCYEKE	QQTVTQLRQM
1150	1160	1170	1180	1190	1200
LENQKNSSVP	LAEHLQVKEA	FEKEVGI <del>II</del> KA	SLREKEEESQ	NKTEEVSKLQ	SEIQNTKQAL
1210	1220	1230	1240	1250	1260
KKLETREVVD	LSKYKATKSD	LETQISDLNE	KLANLNRKYE	EVCEEVLHAK	KKELSAKDEK
1270	1280	1290	1300	1310	1320
ELLHFSIEQE	IKDQQERC <del>DK</del>	SLTTITELQR	RIQESAKQIE	AKDNKITELL	NDVERLKQAL
1330	1340	1350	1360	1370	1380
NGLSQLTYGS	GPS <del>SKR</del> QSQL	IDSLQQQVRS	LQQQLADADR	QHQEVIAIYR	THLLSAAQGH
1390	1400				
MDEDVQAALL	QIIQMRQGLV	C			

Q8HYY4 in FASTA  
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